09/780,525

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     (FILE 'HOME' ENTERED AT 09:48:48 ON 31 JAN 2005)

     FILE 'REGISTRY' ENTERED AT 09:48:57 ON 31 JAN 2005
L1             0 S (TYADFIAS)/SQSP AND 8-15/SQL
L2            12 S (TYADFIAS)/SQSP AND 20/SQL

     FILE 'CAPLUS' ENTERED AT 09:50:36 ON 31 JAN 2005
L3            44 S L2
L4             4 S L3 AND LIBRAR?

     FILE 'STNGUIDE' ENTERED AT 10:03:34 ON 31 JAN 2005

     FILE 'CAPLUS, EMBASE, BIOSIS, MEDLINE, WPIDS' ENTERED AT 10:07:16 ON 31
     JAN 2005

     FILE 'REGISTRY' ENTERED AT 10:07:23 ON 31 JAN 2005
L5             5 S (TYADFIAS)/SQSFP AND 8-15/SQL

     FILE 'CAPLUS, USPATFULL' ENTERED AT 10:08:22 ON 31 JAN 2005
L6             5 S L5

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L4 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:251877 CAPLUS
DN 136:274279
TI Genetic selection method of screening random peptide **libraries** to identify inhibitors of cAMP-dependent kinase phosphorylation pathways
IN Murray, Andrew W.; Smith, Dana L.; Sorger, Peter K.; Norman, Thea C.
PA The Regents of the University of California, USA
SO U.S., 39 pp., Cont.-in-part of U.S. Ser. No. 835,727, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6365347	B1	20020402	US 1998-58483	19980410
PRAI US 1997-835727	B2	19970411		

AB Claimed is a method for constructing macromol. **libraries** by transforming host cells with a collection of recombinant vectors that encode chimeras comprised of a carrier protein and a random peptide sequence, with genetic selection serving to elucidate mols. of diagnostic or therapeutic use. More specifically, it involves screening peptide **libraries** to identify inhibitors of cAMP-dependent kinase phosphorylation pathways. The chimeric gene is expressed intracellularly so that peptide inhibitors of biol. pathways are identified through genetic selection. The cell survives or proliferates when the interaction disrupts the biol. pathway and the cell dies or fails to proliferate when the interaction does not disrupt the biol. pathway. The peptide sequence are placed in the surface loop of the carrier protein, making it conformationally restricted and better able to interact with binding partners with higher affinity than unconstrained peptides. Peptides having a wide variety of uses such as therapeutic of diagnostic reagents, may thus be identified without any prior information on the structure of the desired target for the chimera. Target mols. identified using this method include G-protein coupled receptor of the yeast pheromone pathway, p34cdc2 protein kinase inhibitor of the cell cycle arrest pathway, cdc5-ad protein kinase inhibitor of the cellular DNA damage check point pathway and Mps1 protein kinase inhibitor of the cellular spindle assembly checkpoint pathway.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1999:397274 CAPLUS
DN 131:196233
TI Delineation of selective cyclic GMP-dependent protein kinase Iα substrate and inhibitor peptides based on combinatorial peptide **libraries** on paper
AU Dostmann, Wolfgang R. G.; Nickl, Christian; Thiel, Stefan; Tsigelny, Igor; Frank, Ronald; Tegge, Werner J.
CS Department of Pharmacology, College of Medicine, University of Vermont, Burlington, VT, 05405, USA
SO Pharmacology & Therapeutics (1999), 82(2-3), 373-387
CODEN: PHTHDT; ISSN: 0163-7258
PB Elsevier Science Inc.
DT Journal
LA English
AB Peptide **libraries** on cellulose paper have proven to be valuable tools for the a priori determination of substrate specificities of cAMP- and cyclic GMP-dependent protein kinases (cAMP-kinase and cGMP-kinase) on the basis of octapeptide sequences. Here, we report the extension of our peptide **library** screens to 12-mer and 14-mer peptide sequences, resulting in highly cGMP-kinase Iα selective peptides. The sequences TQAKRKKSLAMA-amide and TQAKRKKSLAMFLR-amide, with Km values for

cGMP-kinase Iα of 0.7 and 0.26 μM and Vmax values of 11.5 and 10.9 μmol/min/mg, resp., display a high specificity for this enzyme. Furthermore, replacing the phosphate acceptor residue serine with alanine in TQAKRKKSLAMA-amide resulted in the highly cGMP-kinase Iα selective inhibitor peptide TQAKRKKALAMA-amide, with inhibitor consts. for cGMP-kinase Iα and cAMP-kinase of 7.5 μM and 750 μM, resp. Selective cGMP-kinase inhibitors have the potential to play an important role in the elucidation of the distinct cellular functions of cGMP-kinase sep. from those activated by cAMP-kinases, and, therefore, may play an important role as pharmaceutical targets. Mol. docking expts. of the most cGMP-kinase selective sequences on a mol. model of the catalytic domain of cGMP-kinase Iα suggest that they adopt unique conformations, which differ significantly from those observed for the cAMP-kinase-specific inhibitor PKI(5-24). Our results suggest that despite their structural similarities, cAMP-kinase and cGMP-kinase use distinct peptide substrate and inhibitor conformations, which could account for their unique substrate specificities. These findings are further supported by cAMP- and cGMP-kinase-selective inhibitor analogs with (D)-Ala residues at the inhibitory positions.

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1997:697439 CAPLUS
DN 128:58871
TI Construction and functional study of protein kinase inhibitor phage
AU Chen, Changzheng; Yang, Xinying; Xia, Qichang; Li, Boliang; Wang, Yinglai
CS Shanghai Institute Biochemistry, Chinese Academy Sciences, Shanghai, 200031, Peop. Rep. China
SO Shengwu Huaxue Yu Shengwu Wuli Xuebao (1997), 29(2), 192-199
CODEN: SHWPAU; ISSN: 0582-9879
PB Shanghai Kexue Jishu Chubanshe
DT Journal
LA Chinese
AB A DNA fragment, which encoded the heat-stable protein kinase inhibitor (PKI) (5-24) of cAMP-dependent protein kinase (cAPK), was synthesized and cloned into phage display vector fd-tet-DOG1. PKI(5-24) was displayed on the surface of phage fd, which was termed PKI phage (cAPK inhibitor phage), in a form fused with gene III protein (g3p). The PKI phage not only repressed cAPK effectively, but also bound with the immobilized recombinant His6-tag mouse cAPK-Cα (His6-mCα) specifically. The bound PKI phages were quant. eluted under acidic conditions. Model affinity screening demonstrated that PKI phages were selectively enriched from the mixture of PKI phages and wild-type phages (1:108) using affinity chromatog. of immobilized His6-mCα. The results suggest that selecting protein kinase inhibitor by phage display technique is feasible.

L4 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1995:960192 CAPLUS
DN 124:9464
TI Modular design and synthesis of oxazolone-derived molecules.
IN Hogan, Joseph C., Jr.; Casebier, David; Furth, Paul; Tu, Cheng
PA Arqule Partners, L.P., USA
SO PCT Int. Appl., 173 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9517903	A1	19950706	WO 1993-US12591	19931228

W: AU, BB, BG, BR, BY, CA, CZ, FI, HU, JP, KR, KZ, LK, LV, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, UZ
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,

BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

CA 2179984	AA	19950706	CA 1993-2179984	19931228
AU 9460499	A1	19950717	AU 1994-60499	19931228
EP 738155	A1	19961023	EP 1994-907107	19931228
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
CN 1105353	A	19950719	CN 1993-121726	19931230
PRAI WO 1993-US12591		19931228		

AB AX[NHCRR1COG]nYB [A, B = bond, H, electrophilic or nucleophilic group, amino acid, nucleotide, or carbohydrate derivative, organic structural motif, reporter element, polymerizable organic group, macromol. component, R; A and B are optionally connected to each other or to other structures; X, Y = bond, ≥1 C, N, S, O atom or combinations thereof; R, R1 = A, B, cyano, NO2, halo, O, OH, alkoxy, thio, alkyl, (substituted) (hetero)aryl, etc.; G = connecting group, bond; n ≥1; with provisos], were prepared The new mols. and fabricated materials are mol. recognition agents useful in the design and synthesis of drugs, and have applications in sepns. and materials science. Thus, oligomer (I; Q1 = 4-benzoylcytidinyl; Q2 = 4-benzoyladeninyl) was prepared in several steps using 2-phenyl-5-oxazolone.

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L3 ANSWER 8 OF 44 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:251877 CAPLUS
DN 136:274279
TI Genetic selection method of screening random peptide libraries to identify inhibitors of cAMP-dependent kinase phosphorylation pathways
IN Murray, Andrew W.; Smith, Dana L.; Sorger, Peter K.; Norman, Thea C.
PA The Regents of the University of California, USA
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CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6365347	B1	20020402	US 1998-58483	19980410
PRAI US 1997-835727	B2	19970411		

RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

WEST Search History

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DATE: Monday, January 31, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR	
☐	L12	(lambda)near2(repressor$)near2(reconstit$)	2
☐	L11	L10 and (DNA)near2(binding)near2(domain$)	58
☐	L10	(peptide$) and (epitope)near2(binding) and (lambda)near2(repressor$)	114
☐	L9	L8 and (lambda)near2(repressor$)	3
☐	L8	L7 and (l2).clm.	53
☐	L7	(l3).clm.	630
☐	L6	L5 and (assay$ or sreen$).clm.	9
☐	L5	L4 and (lambda)near2(repressor$)	133
☐	L4	L3 and l2 and l1	5799
☐	L3	(DNA)near2(binding)near2(domain$)	10166
☐	L2	(protein)near2(peptide) or (epitope)near2(bind or binding)	70613
☐	L1	(two)near2(hybrid)	17013

END OF SEARCH HISTORY

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